

SCORE Search Results Details for Application 10751113 and Search Result us-10-751-113-3.rge.

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OM nucleic - nucleic search, using sw model

Run on: July 25, 2006, 13:42:05 ; Search time 1996 Seconds
(without alignments)
1601.889 Million cell updates/sec

Title: US-10-751-113-3
Perfect score: 50
Sequence: 1 tgccatgtgatactccagga.....actatttccaatgatgatga 50

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_env:*
2: gb_pat:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
7: gb_sts:*
8: gb_sy:*
9: gb_un:*
10: gb_vi:*
11: gb_ov:*
12: gb_htg:*
13: gb_in:*
14: gb_om:*
15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	27.8	55.6	480	2 CQ712958	CQ712958 Sequence
2	27.8	55.6	4495	2 CS162240	CS162240 Sequence

3	27.8	55.6	4495	5	AF010227	AF010227 Homo sapi
4	27.8	55.6	4668	5	AF016031	AF016031 Homo sapi
5	27.8	55.6	4807	5	BC092516	BC092516 Homo sapi
6	27.8	55.6	5256	5	AB209863	AB209863 Homo sapi
7	27.8	55.6	6754	2	CS032155	CS032155 Sequence
8	27.8	55.6	6754	2	CS032413	CS032413 Sequence
9	27.8	55.6	6754	2	CS032417	CS032417 Sequence
10	27.8	55.6	6754	2	CS041107	CS041107 Sequence
11	27.8	55.6	6754	2	CS041365	CS041365 Sequence
12	27.8	55.6	6754	2	CS041369	CS041369 Sequence
13	27.8	55.6	6754	2	CS050236	CS050236 Sequence
14	27.8	55.6	6754	2	AX821998	AX821998 Sequence
15	27.8	55.6	6754	5	AF036892	AF036892 Homo sapi
16	27.8	55.6	6755	2	CQ730100	CQ730100 Sequence
17	27.8	55.6	6832	2	AX384818	AX384818 Sequence
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19	27.8	55.6	6835	2	CS036227	CS036227 Sequence
20	27.8	55.6	6835	2	CS045179	CS045179 Sequence
21	27.8	55.6	6835	2	AR316837	AR316837 Sequence
22	27.8	55.6	6835	5	AF012108	AF012108 Homo sapi
23	27.8	55.6	7994	2	CS032415	CS032415 Sequence
24	27.8	55.6	7994	2	CS041367	CS041367 Sequence
25	27.8	55.6	8207	2	AX780089	AX780089 Sequence
26	27.8	55.6	8207	2	AX780090	AX780090 Sequence
c 27	27.6	55.2	80086	4	AP003290	AP003290 Oryza sat
c 28	27.6	55.2	88558	4	CNS07YPG	AL713935 Oryza sat
29	27.6	55.2	90750	4	AP003797	AP003797 Oryza sat
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35	27.6	55.2	110000	4	AP008218_213	Continuation (214
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c 40	27.6	55.2	110000	4	AP008207_131	Continuation (132
c 41	27.6	55.2	110000	4	AP008207_134	Continuation (135
c 42	27.6	55.2	110000	4	AP008207_336	Continuation (337
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ALIGNMENTS

RESULT 1

CQ712958

LOCUS CQ712958 480 bp DNA linear PAT 03-FEB-2004

DEFINITION Sequence 57884 from Patent WO02070737.

ACCESSION CQ712958

VERSION CQ712958.1 GI:42273815

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1

AUTHORS Liew,C.C., Marshall,W.E. and Zhang,H.

TITLE Compositions and methods relating to osteoarthritis

JOURNAL Patent: WO 02070737-A 57884 12-SEP-2002;

Chondrogene Inc. (CA)

FEATURES

Location/Qualifiers

source

1..480

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

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Query Match 55.6%; Score 27.8; DB 2; Length 480;

Best Local Similarity 82.1%; Pred. No. 14;

Matches 32; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 12 ACTCCAGGACAAGGGAAAACTATTTCCAATGATGATGA 50
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Db 396 AATAAAGAGGCAAGGAAAACTATTTCCAATGATGATGA 434

RESULT 2

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CS162240
LOCUS          CS162240                4495 bp    DNA        linear    PAT 21-SEP-2005
DEFINITION     Sequence 481 from Patent WO2005083429.
ACCESSION      CS162240
VERSION        CS162240.1  GI:76060367
KEYWORDS       .
SOURCE         Homo sapiens (human)
               ORGANISM  Homo sapiens
                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                   Hominidae; Homo.
REFERENCE      1
AUTHORS        Wang, Y.
TITLE          Breast cancer prognostics
JOURNAL        Patent: WO 2005083429-A 481 09-SEP-2005;
               Veridex, LLC (US)
FEATURES       Location/Qualifiers
               source          1..4495
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                               /mol_type="unassigned DNA"
                               /db_xref="taxon:9606"

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Query Match 55.6%; Score 27.8; DB 2; Length 4495;
Best Local Similarity 82.1%; Pred. No. 14;
Matches 32; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 12 ACTCCAGGACAAGGAAAACTATTTCCAATGATGATGA 50
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Db 328 AATAAAGAGCAAGGAAAACTATTTCCAATGATGATGA 366

RESULT 3

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AF010227
LOCUS      AF010227                4495 bp    mRNA    linear    PRI 13-AUG-1997
DEFINITION Homo sapiens receptor-associated coactivator 3 (RAC3) mRNA,
            complete cds.
ACCESSION  AF010227
VERSION    AF010227.1  GI:2318005
KEYWORDS   .
SOURCE     Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE  1 (bases 1 to 4495)
AUTHORS    Li,H., Gomes,P.J. and Chen,J.D.
  TITLE     RAC3, a steroid/nuclear receptor-associated coactivator that is
            related to SRC-1 and TIF2
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 94 (16), 8479-8484 (1997)
  PUBMED   9238002
REFERENCE  2 (bases 1 to 4495)
AUTHORS    Chen,J.D., Li,H. and Gomes,P.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-JUN-1997) Pharmacology and Molecular Toxicology,
            University of Massachusetts Medical School, 55 Lake Avenue North,
            Worcester, MA 01655-0126, USA
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    source          1..4495
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                   /mol_type="mRNA"
                   /db_xref="taxon:9606"
                   /cell_line="HeLa"
    gene            1..4495
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    CDS             86..4339
                   /gene="RAC3"
                   /note="transcriptional coactivator with intrinsic
                   >histone acetyltransferase activity; member of the
                   steroid/nuclear receptor-associated coactivator family

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which includes steroid receptor coactivator 1 (SRC-1), transcriptional intermediate factor 2 (TIF2), and receptor associated coactivator 3; similar to the mouse p300/CBP/co-integrator protein (p/CIP) and the activator of retinoid receptors (ACTR)"

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ORIGIN

Query Match 55.6%; Score 27.8; DB 5; Length 4495;
Best Local Similarity 82.1%; Pred. No. 14;
Matches 32; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 12 ACTCCAGGACAAGGGAAAACTATTTCCAATGATGATGA 50
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Db 328 AATAAAGAGCAAGGAAAACTATTTCCAATGATGATGA 366

RESULT 4

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AF016031
LOCUS      AF016031                4668 bp    mRNA    linear    PRI 05-NOV-1997
DEFINITION Homo sapiens thyroid hormone receptor activator molecule (TRAM-1)
            mRNA, complete cds.
ACCESSION  AF016031
VERSION    AF016031.1  GI:2584879
KEYWORDS   .
SOURCE     Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE  1  (bases 1 to 4668)
  AUTHORS  Takeshita,A., Cardona,G.R., Koibuchi,N., Suen,C.S. and Chin,W.W.
  TITLE    TRAM-1, A novel 160-kDa thyroid hormone receptor activator
            molecule, exhibits distinct properties from steroid receptor
            coactivator-1
            J. Biol. Chem. 272 (44), 27629-27634 (1997)
  JOURNAL  PUBMED
            9346901
REFERENCE  2  (bases 1 to 4668)
  AUTHORS  Takeshita,A., Cardona,G.R., Koibuchi,N. and Chin,W.W.
  TITLE    Direct Submission
  JOURNAL  Submitted (24-JUL-1997) Medicine, Brigham and Women's Hospital,
            Harvard Medical School, 20 Shattuck Street #905, Boston, MA 02115,
            USA
FEATURES   Location/Qualifiers
  source    1. .4668
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Db 434 AATAAAGAGCAAGGAAAACTATTTCCAATGATGATGA 472

BC092516

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SCHNERCH,A., SCHEIN,J.E., JONES,S.J. and MARRA,M.A.
 CONSRTM Mammalian Gene Collection Program Team
 TITLE Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 PUBMED 12477932
 REFERENCE 2 (bases 1 to 4807)
 AUTHORS .
 CONSRTM NIH MGC Project
 TITLE Direct Submission
 JOURNAL Submitted (04-APR-2005) National Institutes of Health, Mammalian
 Gene Collection (MGC), Bethesda, MD 20892-2590, USA
 REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 COMMENT Contact: MGC help desk
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Sequencing Group at the Stanford Human Genome
 Center, Stanford University School of Medicine, Stanford, CA 94305
 Web site: <http://www-shgc.stanford.edu>
 Contact: (Dickson, Mark) mcd@paxil.stanford.edu
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
 R. M.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAK Plate: 199 Row: b Column: 20
 This clone was selected for full length sequencing because it
 passed the following selection criteria: matched mRNA gi: 32307123.

FEATURES Location/Qualifiers
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 /db_xref="taxon:9606"
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ORIGIN

RESULT 7

ORIGIN

RESULT 8

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CS032413
LOCUS          CS032413                6754 bp    DNA        linear    PAT 10-MAR-2005
DEFINITION     Sequence 1919 from Patent WO2005016962.
ACCESSION      CS032413
VERSION        CS032413.1  GI:60731968
KEYWORDS       .
SOURCE         Homo sapiens (human)
  ORGANISM     Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
               Homnidae; Homo.
REFERENCE      1

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AUTHORS Abbas,A., Clark,H., Ouyang,W., Williams,M.P., Wood,W.I. and Wu,T.D.
 TITLE Compositions and methods for the treatment of immune related diseases
 JOURNAL Patent: WO 2005016962-A 1919 24-FEB-2005; Genentech, Inc. (US)
 FEATURES Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
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Query Match 55.6%; Score 27.8; DB 2; Length 6754;
 Best Local Similarity 82.1%; Pred. No. 14;
 Matches 32; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 12 ACTCCAGGACAAGGAAAACTATTTCCAATGATGATGA 50
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 Db 426 AATAAAAGAGCAAGGAAAACTATTTCCAATGATGATGA 464

RESULT 9

CS032417
 LOCUS CS032417 6754 bp DNA linear PAT 10-MAR-2005
 DEFINITION Sequence 1923 from Patent WO2005016962.
 ACCESSION CS032417
 VERSION CS032417.1 GI:60731970
 KEYWORDS .
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.
 REFERENCE 1
 AUTHORS Abbas,A., Clark,H., Ouyang,W., Williams,M.P., Wood,W.I. and Wu,T.D.
 TITLE Compositions and methods for the treatment of immune related diseases
 JOURNAL Patent: WO 2005016962-A 1923 24-FEB-2005; Genentech, Inc. (US)
 FEATURES Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

ORIGIN

Query Match 55.6%; Score 27.8; DB 2; Length 6754;
 Best Local Similarity 82.1%; Pred. No. 14;
 Matches 32; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 12 ACTCCAGGACAAGGAAAACTATTTCCAATGATGATGA 50
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CS041107
 LOCUS CS041107 6754 bp DNA linear PAT 22-MAR-2005
 DEFINITION Sequence 1661 from Patent WO2005019258.
 ACCESSION CS041107
 VERSION CS041107.1 GI:61848654
 KEYWORDS .
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.
 REFERENCE 1
 AUTHORS Abbas,A., Clark,H., Ouyang,W., Williams,P.M., Wood,W.I. and Wu,T.D.
 TITLE Compositions and methods for the treatment of immune related diseases
 JOURNAL Patent: WO 2005019258-A 1661 03-MAR-2005; Genentech, Inc. (US)
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Matches 32; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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CS041365
LOCUS          CS041365              6754 bp    DNA        linear    PAT 22-MAR-2005
DEFINITION    Sequence 1919 from Patent WO2005019258.
ACCESSION     CS041365
VERSION       CS041365.1   GI:61848857
KEYWORDS      .
SOURCE        Homo sapiens (human)
  ORGANISM    Homo sapiens
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              Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
              Hominidae; Homo.
REFERENCE     1
  AUTHORS     Abbas,A., Clark,H., Ouyang,W., Williams,P.M., Wood,W.I. and Wu,T.D.
  TITLE       Compositions and methods for the treatment of immune related
              diseases
  JOURNAL     Patent: WO 2005019258-A 1919 03-MAR-2005;
              Genentech, Inc. (US)
FEATURES             Location/Qualifiers
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ORIGIN

Query Match 55.6%; Score 27.8; DB 2; Length 6754;
Best Local Similarity 82.1%; Pred. No. 14;
Matches 32; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 12 ACTCCAGGACAAGGGAAAACTATTTCCAATGATGATGA 50
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Db 426 AATAAAGAGCAAGGAAAACTATTTCCAATGATGATGA 464

RESULT 12

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CS041369
LOCUS          CS041369              6754 bp    DNA        linear    PAT 22-MAR-2005
DEFINITION     Sequence 1923 from Patent WO2005019258.
ACCESSION      CS041369
VERSION        CS041369.1  GI:61848859
KEYWORDS       .
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
               Hominidae; Homo.
REFERENCE      1
AUTHORS        Abbas,A., Clark,H., Ouyang,W., Williams,P.M., Wood,W.I. and Wu,T.D.
TITLE          Compositions and methods for the treatment of immune related
               diseases
JOURNAL        Patent: WO 2005019258-A 1923 03-MAR-2005;
               Genentech, Inc. (US)
FEATURES       Location/Qualifiers
               source                1. .6754
                                   /organism="Homo sapiens"
                                   /mol_type="unassigned DNA"
                                   /db_xref="taxon:9606"

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ORIGIN

Query Match 55.6%; Score 27.8; DB 2; Length 6754;
Best Local Similarity 82.1%; Pred. No. 14;
Matches 32; Conservative 0; Mismatches 7; Indels 0; Gaps 0;


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ACCESSION      AF036892
VERSION        AF036892.1  GI:2707769
KEYWORDS       .
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                Hominidae; Homo.
REFERENCE      1  (bases 1 to 6754)
AUTHORS        Chen,H., Lin,R.J., Schiltz,R.L., Chakravarti,D., Nash,A., Nagy,L.,
                Privalsky,M.L., Nakatani,Y. and Evans,R.M.
TITLE          Nuclear receptor coactivator ACTR is a novel histone
                acetyltransferase and forms a multimeric activation complex with
                P/CAF and CBP/p300
JOURNAL        Cell 90 (3), 569-580 (1997)
PUBMED        9267036
REFERENCE      2  (bases 1 to 6754)
AUTHORS        Chen,H. and Evans,R.M.
TITLE          Direct Submission
JOURNAL        Submitted (03-DEC-1997) Gene Expression Lab, The Salk Institute for
                Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
                USA

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ORIGIN

Qy 12 ACTCCAGGACAAGGGAAAACTATTTCCAATGATGATGA 50
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Db 426 AATAAAGAGCAAGGAAAACTATTTCCAATGATGATGA 464

Search completed: July 25, 2006, 14:15:31
Job time : 1998 secs

SCORE 1.3 BuildDate: 12/06/2005

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c	12	24.2	48.4	529885	3	US-09-949-016-14342	Sequence 14342, A
c	13	24.2	48.4	529885	3	US-09-949-016-14343	Sequence 14343, A
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	27	22.4	44.8	601	3	US-09-949-016-61449	Sequence 61449, A
	28	22.4	44.8	601	3	US-09-949-016-67687	Sequence 67687, A
	29	22.4	44.8	1194	3	US-10-243-468-1	Sequence 1, Appli
c	30	22.4	44.8	2065	4	US-10-094-749-1293	Sequence 1293, Ap
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	32	22.4	44.8	206433	3	US-09-949-016-13527	Sequence 13527, A
	33	22.4	44.8	254778	3	US-09-949-016-12417	Sequence 12417, A
c	34	22.2	44.4	601	3	US-09-949-016-182740	Sequence 182740, A
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	36	22.2	44.4	1689	3	US-09-903-190-61	Sequence 61, Appli
	37	22.2	44.4	1746	3	US-08-951-130-5	Sequence 5, Appli
	38	22.2	44.4	1746	3	US-09-430-806A-5	Sequence 5, Appli
	39	22.2	44.4	1860	3	US-09-895-652A-4	Sequence 4, Appli
	40	22.2	44.4	2607	2	US-08-369-796-5	Sequence 5, Appli
	41	22.2	44.4	2607	2	US-08-852-091-5	Sequence 5, Appli
	42	22.2	44.4	2607	2	US-08-820-754-5	Sequence 5, Appli
	43	22.2	44.4	2607	3	US-08-956-652-5	Sequence 5, Appli
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	45	22.2	44.4	2607	3	US-08-948-547-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1

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US-09-949-016-4981
; Sequence 4981, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4981
; LENGTH: 6760
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-4981

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Query Match 55.6%; Score 27.8; DB 3; Length 6760;
Best Local Similarity 82.1%; Pred. No. 0.93;
Matches 32; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 12 ACTCCAGGACAAGGGAAAACTATTTCCAATGATGATGA 50
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Db 424 AATAAAGAGCAAGGAAAACTATTTCCAATGATGATGA 462

RESULT 2

US-09-125-635-1

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; Sequence 1, Application US/09125635
; Patent No. 6562589
; GENERAL INFORMATION:
; APPLICANT: THE UNITED STATES OF AMERICA represented by THE SE
; TITLE OF INVENTION: AIB1, A novel steroid receptor co-activator
; FILE REFERENCE: 49944
; CURRENT APPLICATION NUMBER: US/09/125,635
; CURRENT FILING DATE: 1998-08-21
; PRIOR APPLICATION NUMBER: 60/049,728
; PRIOR FILING DATE: 1997-06-17
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 6835
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (201)..(4463)
US-09-125-635-1
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Query Match          55.6%; Score 27.8; DB 3; Length 6835;
Best Local Similarity 82.1%; Pred. No. 0.93;
Matches 32; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
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RESULT 3

US-09-949-016-16723

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; Sequence 16723, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
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; SEQ ID NO 16723
; LENGTH: 157822
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16723
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RESULT 4

US-09-125-635-9

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; Sequence 9, Application US/09125635
; Patent No. 6562589
; GENERAL INFORMATION:
; APPLICANT: THE UNITED STATES OF AMERICA represented by THE SE
; TITLE OF INVENTION: AIB1, A novel steroid receptor co-activator
; FILE REFERENCE: 49944
; CURRENT APPLICATION NUMBER: US/09/125,635
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; CURRENT FILING DATE: 1998-08-21
; PRIOR APPLICATION NUMBER: 60/049,728
; PRIOR FILING DATE: 1997-06-17
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 4621
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (110)..(4318)
US-09-125-635-9
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Db      355 AATAAAGAACAAGGGAAAACTATTTCCAGTGATGATGA 393
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RESULT 5

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US-09-445-353E-1
; Sequence 1, Application US/09445353E
; Patent No. 6812336
; GENERAL INFORMATION:
; APPLICANT: Rosenfeld, Michael G.
; APPLICANT: Glass, Christopher K.
; APPLICANT: Rose, David W.
; APPLICANT: Torchia, Joseph
; TITLE OF INVENTION: A Transcription Factor Coactivator Protein, p/CIP
; FILE REFERENCE: 6627-PA1021
; CURRENT APPLICATION NUMBER: US/09/445,353E
; CURRENT FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: PCT/US98/12263
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: 60/049,452
; PRIOR FILING DATE: 1997-06-12
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 4860
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (3121)..(3121)
; OTHER INFORMATION: "n" is any nucleotide
; NAME/KEY: CDS
; LOCATION: (110)..(4318)
; OTHER INFORMATION:
; PUBLICATION INFORMATION:
; AUTHORS: Joseph Torchia, David W. Rose, Juan Inostroza, Yasutomi Kamei,
; AUTHORS: Stefan Westin
; TITLE: The transcriptional co-activator p/CIP binds CBP and mediates
; TITLE: nuclear receptor function
; JOURNAL: Nature
; VOLUME: 387
; ISSUE: 6634
; PAGES: 677-684
; DATE: 1997-06-12
; DATABASE ACCESSION NUMBER: AF000581
; DATABASE ENTRY DATE: 1997-06-12
US-09-445-353E-1
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Best Local Similarity 79.5%; Pred. No. 3.5;
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RESULT 6

US-09-949-016-16928/c
; Sequence 16928, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16928
; LENGTH: 524032
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(524032)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16928

Query Match 48.4%; Score 24.2; DB 3; Length 524032;
Best Local Similarity 71.1%; Pred. No. 62;
Matches 32; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 5 ATGTGATACTCCAGGACAAGGGAAAACTATTTC CAATGATGATG 49
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Db 121801 ATGTAATTCTCCAGAATAAGAAAAAATCTATT TGGCAAGCTAATG 121757

RESULT 7

US-09-949-016-16929/c
; Sequence 16929, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16929
; LENGTH: 524032
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(524032)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16929

Query Match 48.4%; Score 24.2; DB 3; Length 524032;
Best Local Similarity 71.1%; Pred. No. 62;
Matches 32; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 5 ATGTGATACTCCAGGACAAGGGAAAACTATTTC CAATGATGATG 49
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Db 121801 ATGTAATTCTCCAGAATAAGAAAAAATCTATT TGGCAAGCTAATG 121757

SCORE Search Results Details for Application 10751113 and Search Result us-10-751-113-3.rnpbm.

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OM nucleic - nucleic search, using sw model

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Maximum Match 100%
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- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
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- 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
- 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	27.8	55.6	480	8	US-10-085-783A-57884	Sequence 57884, A
4	27.8	55.6	4263	7	US-10-414-692-35	Sequence 35, Appl
5	27.8	55.6	6754	7	US-10-388-360-376	Sequence 376, App
6	27.8	55.6	6754	7	US-10-159-563-346	Sequence 346, App
7	27.8	55.6	6754	10	US-10-504-173-126	Sequence 126, App
8	27.8	55.6	6832	9	US-10-333-894A-18	Sequence 18, Appl
9	27.8	55.6	6835	7	US-10-379-616-1	Sequence 1, Appli
10	27.8	55.6	6845	7	US-10-418-027-2	Sequence 2, Appli
11	27.8	55.6	7116	7	US-10-252-157-198	Sequence 198, App
12	27.6	55.2	34	9	US-10-751-113-2	Sequence 2, Appli
13	27.6	55.2	591	12	US-10-301-480-372333	Sequence 372333,
14	27.6	55.2	591	12	US-10-301-480-985742	Sequence 985742,
15	27.6	55.2	595	4	US-09-925-065A-295471	Sequence 295471,
16	27.6	55.2	595	5	US-09-925-065A-295471	Sequence 295471,
17	26.4	52.8	403	3	US-09-918-995-3925	Sequence 3925, Ap
c 18	26.4	52.8	137671	15	US-11-121-086-47	Sequence 47, Appl
c 19	26.4	52.8	268685	7	US-10-265-071-22	Sequence 22, Appl
c 20	26.4	52.8	268685	7	US-10-025-966A-22	Sequence 22, Appl
c 21	26.4	52.8	268685	10	US-10-933-025-22	Sequence 22, Appl
c 22	26.4	52.8	268685	16	US-11-219-360-22	Sequence 22, Appl
c 23	26.2	52.4	394	8	US-10-424-599-130512	Sequence 130512,
24	26.2	52.4	4621	7	US-10-379-616-9	Sequence 9, Appli
25	26.2	52.4	4860	10	US-10-971-982-1	Sequence 1, Appli
26	25	50.0	35	9	US-10-751-113-1	Sequence 1, Appli
27	24.8	49.6	888	9	US-10-767-795-4182	Sequence 4182, Ap
28	24.8	49.6	1838	8	US-10-424-599-102375	Sequence 102375,
29	24.6	49.2	600	10	US-10-972-079-27987	Sequence 27987, A
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c 34	24.4	48.8	171936	7	US-10-025-966A-24	Sequence 24, Appl
c 35	24.4	48.8	171936	10	US-10-933-025-24	Sequence 24, Appl
c 36	24.4	48.8	171936	16	US-11-219-360-24	Sequence 24, Appl
37	24.2	48.4	600	10	US-10-972-079-94644	Sequence 94644, A
c 38	23.8	47.6	864	8	US-10-282-122A-24678	Sequence 24678, A
c 39	23.8	47.6	1191	4	US-09-925-065A-27117	Sequence 27117, A
c 40	23.8	47.6	1191	5	US-09-925-065A-27117	Sequence 27117, A
c 41	23.8	47.6	1191	12	US-10-301-480-128354	Sequence 128354,
c 42	23.8	47.6	1191	12	US-10-301-480-741763	Sequence 741763,
c 43	23.8	47.6	10199	8	US-10-398-221-3885	Sequence 3885, Ap
c 44	23.8	47.6	169659	8	US-10-322-696-70	Sequence 70, Appl
45	23.8	47.6	2944528	16	US-11-045-004-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-10-751-113-3

; Sequence 3, Application US/10751113

; Publication No. US20040259114A1

; GENERAL INFORMATION:

; APPLICANT: RIEGEL, ANNA T.

; APPLICANT: REITER, RONALD

; APPLICANT: WELLSTEIN, ANTON

; TITLE OF INVENTION: COACTIVATORS IN THE DIAGNOSIS AND TREATMENT OF BREAST

; TITLE OF INVENTION: CANCER

; FILE REFERENCE: 54458-20001.00

; CURRENT APPLICATION NUMBER: US/10/751,113

; CURRENT FILING DATE: 2004-01-05

; PRIOR APPLICATION NUMBER: PCT/US02/21066

; PRIOR FILING DATE: 2002-07-03

; PRIOR APPLICATION NUMBER: 60/302,648

; PRIOR FILING DATE: 2001-07-05

; NUMBER OF SEQ ID NOS: 3

; SOFTWARE: PatentIn Ver. 3.2

; SEQ ID NO 3

; LENGTH: 50

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-751-113-3

Query Match 100.0%; Score 50; DB 9; Length 50;

Best Local Similarity 100.0%; Pred. No. 1.6e-08;

Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 TGCCATGTGATACTCCAGGACAAGGGAAAACTATTTCCAATGATGATGA 50
        |||||
Db      1 TGCCATGTGATACTCCAGGACAAGGGAAAACTATTTCCAATGATGATGA 50
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RESULT 2

US-10-242-535A-57884

; Sequence 57884, Application US/10242535A

; Publication No. US20040013663A1

; GENERAL INFORMATION:

; APPLICANT: ChondroGene Inc.

; APPLICANT: Liew, C.C.

; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis

; FILE REFERENCE: 4231/2005

; CURRENT APPLICATION NUMBER: US/10/242,535A

; CURRENT FILING DATE: 2002-09-12

; PRIOR APPLICATION NUMBER: US 10/085,783

; PRIOR FILING DATE: 2002-02-28

; PRIOR APPLICATION NUMBER: US 60/305,340

; PRIOR FILING DATE: 2001-07-13

; PRIOR APPLICATION NUMBER: US 60/275,017

; PRIOR FILING DATE: 2001-03-12

; PRIOR APPLICATION NUMBER: US 60/271,955

; PRIOR FILING DATE: 2001-02-28

; NUMBER OF SEQ ID NOS: 58994

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 57884

; LENGTH: 480

; TYPE: DNA

; ORGANISM: Human

US-10-242-535A-57884

Query Match 55.6%; Score 27.8; DB 8; Length 480;

Best Local Similarity 82.1%; Pred. No. 5.5;

Matches 32; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Qy      12 ACTCCAGGACAAGGGAAAACTATTTCCAATGATGATGA 50
        |||||
Db      396 AATAAAGAGCAAGGAAAACTATTTCCAATGATGATGA 434
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RESULT 3

US-10-085-783A-57884

; Sequence 57884, Application US/10085783A

; Publication No. US20040037841A1

; GENERAL INFORMATION:

; APPLICANT: ChondroGene Inc.

; APPLICANT: Liew, C.C.

; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis

; FILE REFERENCE: 4231/2002

; CURRENT APPLICATION NUMBER: US/10/085,783A

; CURRENT FILING DATE: 2002-02-28

; PRIOR APPLICATION NUMBER: US 60/305,340

; PRIOR FILING DATE: 2001-07-13

; PRIOR APPLICATION NUMBER: US 60/275,017

; PRIOR FILING DATE: 2001-03-12

; PRIOR APPLICATION NUMBER: US 60/271,955

; PRIOR FILING DATE: 2001-02-28

; NUMBER OF SEQ ID NOS: 58994

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 57884

; LENGTH: 480

; TYPE: DNA

; ORGANISM: Human

US-10-085-783A-57884

Query Match 55.6%; Score 27.8; DB 8; Length 480;

Best Local Similarity 82.1%; Pred. No. 5.5;

Matches 32; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Qy      12 ACTCCAGGACAAGGGAAAACTATTTCCAATGATGATGA 50
        |||||
Db      396 AATAAAGAGCAAGGAAAACTATTTCCAATGATGATGA 434
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RESULT 4

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US-10-414-692-35
; Sequence 35, Application US/10414692
; Publication No. US20030228607A1
; GENERAL INFORMATION:
; APPLICANT: X-Cepto Therapeutics, Inc.
; TITLE OF INVENTION: Screening method and modulators having an improved therapeutic
; TITLE OF INVENTION: profile
; FILE REFERENCE: 8012-002-US
; CURRENT APPLICATION NUMBER: US/10/414,692
; CURRENT FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: 60/372,650
; PRIOR FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 35
; LENGTH: 4263
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-414-692-35
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Query Match 55.6%; Score 27.8; DB 7; Length 4263;
Best Local Similarity 82.1%; Pred. No. 9.3;
Matches 32; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 12 ACTCCAGGACAAGGGAAAACTATTTCCAATGATGATGA 50
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Db 243 AATAAAGAGCAAGGAAAACTATTTCCAATGATGATGA 281

RESULT 5

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US-10-388-360-376
; Sequence 376, Application US/10388360
; Publication No. US20030225528A1
; GENERAL INFORMATION:
; APPLICANT: GENOMIC HEALTH
; APPLICANT: Baker, Joffre B.
; APPLICANT: Cronin, Maureen T.
; APPLICANT: Kiefer, Michael C.
; APPLICANT: Shak, Steve
; APPLICANT: Walker, Michael Graham
; TITLE OF INVENTION: GENE EXPRESSION PROFILING IN BIOPSIED TUMOR TISSUES
; FILE REFERENCE: 39740-0001US
; CURRENT APPLICATION NUMBER: US/10/388,360
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 60/412,049
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: US 60/364,890
; PRIOR FILING DATE: 2002-03-13
; NUMBER OF SEQ ID NOS: 384
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 376
;   LENGTH: 6754
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-388-360-376

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Query Match 55.6%; Score 27.8; DB 7; Length 6754;
Best Local Similarity 82.1%; Pred. No. 10;
Matches 32; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 12 ACTCCAGGACAAGGGAAAACTATTTCCAATGATGATGA 50
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Db 426 AATAAAGAGCAAGGAAAACTATTTCCAATGATGATGA 464

RESULT 6

US-10-159-563-346
; Sequence 346, Application US/10159563
; Publication No. US20040009154A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Javed
; APPLICANT: Ringner, Markus
; APPLICANT: Peterson, Carsten
; APPLICANT: Meltzer, Paul

```
; TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR
; TITLE OF INVENTION: DIAGNOSIS AND FOR TARGETING THE THERAPY OF SELECT CANCERS
; FILE REFERENCE: 11613.56US11
; CURRENT APPLICATION NUMBER: US/10/159,563
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 10/133,937
; PRIOR FILING DATE: 2002-04-25
; NUMBER OF SEQ ID NOS: 444
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 346
; LENGTH: 6754
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-159-563-346
```

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Query Match          55.6%; Score 27.8; DB 7; Length 6754;
Best Local Similarity 82.1%; Pred. No. 10;
Matches 32; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
```

```
Qy      12 ACTCCAGGACAAGGGAAAACTATTTCCAATGATGATGA 50
        | | | | | | | | | | | | | | | | | | | | | |
Db      426 AATAAAAGAGCAAGGAAAACTATTTCCAATGATGATGA 464
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RESULT 7

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US-10-504-173-126
; Sequence 126, Application US/10504173
; Publication No. US20050202428A1
; GENERAL INFORMATION:
; APPLICANT: Axordia Limited
; TITLE OF INVENTION: Pluripotential Stem Cells
; FILE REFERENCE: P101863WO
; CURRENT APPLICATION NUMBER: US/10/504,173
; CURRENT FILING DATE: 2004-08-11
; PRIOR APPLICATION NUMBER: 0203359.5
; PRIOR FILING DATE: 2002-02-02
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 126
; LENGTH: 6754
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-504-173-126
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Query Match          55.6%; Score 27.8; DB 10; Length 6754;
Best Local Similarity 82.1%; Pred. No. 10;
Matches 32; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
```

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Qy      12 ACTCCAGGACAAGGGAAAACTATTTCCAATGATGATGA 50
        | | | | | | | | | | | | | | | | | | | | | |
Db      426 AATAAAAGAGCAAGGAAAACTATTTCCAATGATGATGA 464
```

RESULT 8

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US-10-333-894A-18
; Sequence 18, Application US/10333894A
; Publication No. US20040259085A1
; GENERAL INFORMATION:
; APPLICANT: Chang, Chawnshang
; APPLICANT: Hsing, Ann
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR PREDICTING
; TITLE OF INVENTION: PROSTATE CANCER
; FILE REFERENCE: 21108.0001U1
; CURRENT APPLICATION NUMBER: US/10/333,894A
; CURRENT FILING DATE: 2003-01-24
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 6832
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/note =
; OTHER INFORMATION: synthetic construct
US-10-333-894A-18
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SCORE Search Results Details for Application 10751113 and Search Result us-10-751-113-3.rnpbn.

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OM nucleic - nucleic search, using sw model

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Gapop 10.0 , Gapext 1.0

Searched: 899801 seqs, 718270062 residues

Total number of hits satisfying chosen parameters: 1799602

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	27.8	55.6	7923	8	US-11-283-329-155	Sequence 155, App
2	27.8	55.6	7935	8	US-11-266-748A-56675	Sequence 56675, A
3	27.8	55.6	7935	8	US-11-283-329-153	Sequence 153, App
4	25.2	50.4	789	8	US-11-266-748A-113927	Sequence 113927,
c 5	25.2	50.4	789	8	US-11-266-748A-161615	Sequence 161615,
c 6	22.8	45.6	605	8	US-11-266-748A-80002	Sequence 80002, A
7	22.8	45.6	605	8	US-11-266-748A-132813	Sequence 132813,
8	22.8	45.6	614	8	US-11-266-748A-43663	Sequence 43663, A

	9	22.8	45.6	614	8	US-11-266-748A-209785	Sequence 209785,
	10	22.8	45.6	976	8	US-11-266-748A-354333	Sequence 354333,
c	11	22.8	45.6	976	8	US-11-266-748A-437712	Sequence 437712,
c	12	22.8	45.6	1086	8	US-11-266-748A-75251	Sequence 75251, A
c	13	22.8	45.6	1086	8	US-11-266-748A-108806	Sequence 108806,
	14	22.8	45.6	1086	8	US-11-266-748A-128062	Sequence 128062,
	15	22.8	45.6	2188	8	US-11-266-748A-185432	Sequence 185432,
	16	22.8	45.6	5393	8	US-11-266-748A-22455	Sequence 22455, A
	17	22.8	45.6	5966	8	US-11-266-748A-28012	Sequence 28012, A
c	18	22.6	45.2	1000	8	US-11-266-748A-284293	Sequence 284293,
	19	22.6	45.2	1000	8	US-11-266-748A-335722	Sequence 335722,
c	20	22.6	45.2	1340	6	US-10-953-349-13326	Sequence 13326, A
c	21	22.6	45.2	7011	8	US-11-350-336-9	Sequence 9, Appli
	22	22.4	44.8	1616	8	US-11-266-748A-352261	Sequence 352261,
c	23	22.4	44.8	1616	8	US-11-266-748A-435640	Sequence 435640,
c	24	22.2	44.4	687	8	US-11-266-748A-216355	Sequence 216355,
	25	22.2	44.4	687	8	US-11-266-748A-238191	Sequence 238191,
	26	22.2	44.4	755	8	US-11-266-748A-46670	Sequence 46670, A
	27	22.2	44.4	824	8	US-11-266-748A-163709	Sequence 163709,
	28	22.2	44.4	868	8	US-11-266-748A-14916	Sequence 14916, A
	29	22.2	44.4	1000	8	US-11-266-748A-287318	Sequence 287318,
c	30	22.2	44.4	1000	8	US-11-266-748A-338747	Sequence 338747,
	31	22.2	44.4	1000	8	US-11-266-748A-397979	Sequence 397979,
	32	22.2	44.4	1000	8	US-11-266-748A-404038	Sequence 404038,
c	33	22.2	44.4	1000	8	US-11-266-748A-469025	Sequence 469025,
c	34	22.2	44.4	1000	8	US-11-266-748A-475084	Sequence 475084,
c	35	22.2	44.4	1461	8	US-11-266-748A-192770	Sequence 192770,
c	36	22.2	44.4	1461	8	US-11-266-748A-226616	Sequence 226616,
	37	22.2	44.4	1461	8	US-11-266-748A-240826	Sequence 240826,
	38	22.2	44.4	1701	8	US-11-105-233-2	Sequence 2, Appli
	39	22.2	44.4	1701	8	US-11-105-233-103	Sequence 103, App
	40	22.2	44.4	1916	8	US-11-266-748A-78147	Sequence 78147, A
	41	22.2	44.4	1916	8	US-11-266-748A-110132	Sequence 110132,
c	42	22.2	44.4	1916	8	US-11-266-748A-130958	Sequence 130958,
	43	22.2	44.4	2762	8	US-11-266-748A-31173	Sequence 31173, A
	44	22.2	44.4	3717	8	US-11-266-748A-185976	Sequence 185976,
	45	22.2	44.4	3717	8	US-11-266-748A-193357	Sequence 193357,

ALIGNMENTS

RESULT 1

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US-11-283-329-155
; Sequence 155, Application US/11283329
; Publication No. US20060134670A1
; GENERAL INFORMATION:
; APPLICANT: Piu, Fabrice
; TITLE OF INVENTION: ENABLING TOOLS TO IDENTIFY LIGANDS FOR
; TITLE OF INVENTION: HORMONE NUCLEAR RECEPTORS
; FILE REFERENCE: ACADIA.043A
; CURRENT APPLICATION NUMBER: US/11/283,329
; CURRENT FILING DATE: 2005-11-18
; PRIOR APPLICATION NUMBER: 60/629,811
; PRIOR FILING DATE: 2004-11-19
; NUMBER OF SEQ ID NOS: 242
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 155
; LENGTH: 7923
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (206)...(4468)
; OTHER INFORMATION: SRC-3 variant 2
US-11-283-329-155

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Query Match 55.6%; Score 27.8; DB 8; Length 7923;
Best Local Similarity 82.1%; Pred. No. 0.65;
Matches 32; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 12 ACTCCAGGACAAGGGAAAACTATTTCGAATGATGATGA 50
 | | | | |
Db 448 AATAAAGAGCAAGGAAAACTATTTCGAATGATGATGA 486

RESULT 2

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US-11-266-748A-56675
; Sequence 56675, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 56675
;   LENGTH: 7935
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-11-266-748A-56675

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Query Match 55.6%; Score 27.8; DB 8; Length 7935;
Best Local Similarity 82.1%; Pred. No. 0.65;
Matches 32; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 12 ACTCCAGGACAAGGGAAAACTATTTCCAATGATGATGA 50
 | | | || | |||||
Db 448 AATAAAGAGCAAGGAAAACTATTTCCAATGATGATGA 486

RESULT 3

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US-11-283-329-153
; Sequence 153, Application US/11283329
; Publication No. US20060134670A1
; GENERAL INFORMATION:
; APPLICANT: Piu, Fabrice
; TITLE OF INVENTION: ENABLING TOOLS TO IDENTIFY LIGANDS FOR
; TITLE OF INVENTION: HORMONE NUCLEAR RECEPTORS
; FILE REFERENCE: ACADIA.043A
; CURRENT APPLICATION NUMBER: US/11/283,329
; CURRENT FILING DATE: 2005-11-18
; PRIOR APPLICATION NUMBER: 60/629,811
; PRIOR FILING DATE: 2004-11-19
; NUMBER OF SEQ ID NOS: 242
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 153
; LENGTH: 7935
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (206)...(4480)
; OTHER INFORMATION: SRC-3 variant 1
US-11-283-329-153

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Query Match 55.6%; Score 27.8; DB 8; Length 7935;
Best Local Similarity 82.1%; Pred. No. 0.65;
Matches 32; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 12 ACTCCAGGACAAGGGAAAACTATTTCCAATGATGATGA 50

Db 448 AATAAAAGAGCAAGGAAAACTATTTCCAATGATGATGA 486

RESULT 4

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US-11-266-748A-113927
; Sequence 113927, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 113927
; LENGTH: 789
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-113927

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Query Match 50.4%; Score 25.2; DB 8; Length 789;
Best Local Similarity 71.7%; Pred. No. 3.5;
Matches 33; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 1 TGCCATGTGATACTCCAGGACAAGGGAAAACTATTTCCAATGATG 46
 ||||| || | |||| | | | | | | | | | |
Db 440 TGCCATGATGTACGCCAGGCCAAAGGACAAGCCAGGTCGCATGATG 485

RESULT 5

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US-11-266-748A-161615/c
; Sequence 161615, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
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; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276

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; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 161615
; LENGTH: 789
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-161615
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Query Match          50.4%; Score 25.2; DB 8; Length 789;
Best Local Similarity 71.7%; Pred. No. 3.5;
Matches 33; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
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Db      350 TGCCATGATGTACGCCAGGCCAAAGGACAAGCCAGGTCGCATGATG 305
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RESULT 6

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US-11-266-748A-80002/c
; Sequence 80002, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 80002
; LENGTH: 605
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-80002
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Best Local Similarity 71.4%; Pred. No. 28;
Matches 30; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
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Db      364 ATATGAGCCTTTAAACATGGGTAAACTAATCCCATTGATG 323
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RESULT 7

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US-11-266-748A-132813
; Sequence 132813, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
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5	27.8	55.6	537	2	BM146766	BM146766	TCAAP1E73
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8	27.8	55.6	556	9	DB091786	DB091786	DB091786
9	27.8	55.6	557	9	DB134417	DB134417	DB134417
10	27.8	55.6	566	9	DA328439	DA328439	DA328439
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12	27.8	55.6	581	3	BP351331	BP351331	BP351331
13	27.8	55.6	581	3	BP353869	BP353869	BP353869
14	27.8	55.6	582	3	BP280749	BP280749	BP280749
15	27.8	55.6	583	3	BP282535	BP282535	BP282535
16	27.8	55.6	583	3	BP310850	BP310850	BP310850
17	27.8	55.6	583	3	BP315317	BP315317	BP315317
18	27.8	55.6	588	9	DA189529	DA189529	DA189529
19	27.8	55.6	597	9	DA248756	DA248756	DA248756
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22	27.8	55.6	843	5	CD657296	CD657296	AGENCOURT
23	27.6	55.2	908	14	AG891620	AG891620	Oryza sat
24	26.8	53.6	700	7	BB865389	BB865389	BB865389
c 25	26.6	53.2	668	14	DU475651	DU475651	109841573
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c 28	26.2	52.4	394	7	AW153178	AW153178	se36h11.y
29	26.2	52.4	443	5	CF165306	CF165306	B0754H03-
30	26.2	52.4	469	8	CN682253	CN682253	E0161G12-
31	26.2	52.4	581	8	CN682136	CN682136	E0160C01-
32	26.2	52.4	637	7	BB659498	BB659498	BB659498
33	26.2	52.4	660	4	BY751007	BY751007	BY751007
34	26.2	52.4	672	7	BB865764	BB865764	BB865764
35	26.2	52.4	716	4	CB522550	CB522550	UI-M-GH0-
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38	26.2	52.4	5131	6	AK142306	AK142306	Mus muscu
39	26.2	52.4	5237	6	BC086482	BC086482	Mus muscu
40	26	52.0	424	2	BF887288	BF887288	CM4-TN014
c 41	25.8	51.6	714	7	BB648365	BB648365	BB648365
42	25.8	51.6	721	7	BF215672	BF215672	601881152
43	25.6	51.2	671	10	DV096016	DV096016	327-384-5
44	25.6	51.2	755	7	BE394099	BE394099	601312476
c 45	25.6	51.2	830	14	DX265018	DX265018	OR_ABa015

ALIGNMENTS

RESULT 1
CT346760
LOCUS CT346760 499 bp DNA linear GSS 03-NOV-2005
DEFINITION Sus scrofa genomic clone CH242-41J6, genomic survey sequence.
ACCESSION CT346760
VERSION CT346760.1 GI:79916147
KEYWORDS GSS.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.
REFERENCE 1 (bases 1 to 499)
AUTHORS Humphray, S.J., Plumb, R.W. and Durham, J.L.
TITLE Direct Submission
JOURNAL Submitted (01-NOV-2005) The Sanger Institute, Wellcome Trust Genome
Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Unpublished
COMMENT This sequence was generated from the SP6 end of BAC 41J6. 41J6 is
part of the CHORI-242 BAC Library created by P. de Jong. Further
details: http://www.sanger.ac.uk/Projects/S_scrofa/.
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source 1. .499
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/mol_type="genomic DNA"
/db_xref="taxon:9823"
/clone="CH242-41J6"
/tissue_type="White blood cells"
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ORIGIN

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BX643165

KEYWORDS EST.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 230)

TITLE EST (Koehrer, K., Beyer, A., Mewes, H.W., Weil, B., Amid, C., et al.)

JOURNAL Unpublished (2003)

COMMENT Contact: MIPS

FEATURES

source

ORIGIN

Qy 12 ACTCCAGGACAAGGGAAAACTATTTCGAATGATGATGA 50
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Db 104 AATAAAGAGCAAGGAAAACTATTTCGAATGATGATGA 14

DB070018

KEYWORDS EST.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Query Match	55.6%;	Score 27.8;	DB 9;	Length 531;
Best Local Similarity	82.1%;	Pred. No. 43;		
Matches 32;	Conservative	0;	Mismatches 7;	Indels 0; Gaps 0;

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Db 449 AATAAAAGACCAAGGAAAACTATTTC CAATGATGATGA 487

RESULT 4	
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LOCUS	DB060916 532 bp mRNA linear EST 04-DEC-2005
DEFINITION	DB060916 TESTI4 Homo sapiens cDNA clone TESTI4000618 5', mRNA sequence.
ACCESSION	DB060916
VERSION	DB060916.1 GI:83255232
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 532)
AUTHORS	Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T., Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaguri,H., Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N., Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M., Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A., Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.
TITLE	Diversification of Transcriptional Modulation: Large-scale Identification and Characterization of Putative Alternative Promoters of Human Genes
JOURNAL	Genome Res. 16 (1), 55-65 (2006)
PUBMED	16344560
COMMENT	Contact: Takao Isogai FLJ Project (HRI Team) Helix Research Institute 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan Tel: 81-438-52-3975

Email: flj-cdna@nifty.com

NEDO human cDNA project (New Energy and Industrial Technology Developmental Organization, Japan); cDNA library construction: Helix Research Institute (HRI); 5'-end one pass sequencing: HRI, Research Association for Biotechnology (RAB) and Biotechnology Center, National Institute of Technology and Evaluation; 3'-end one pass sequencing: RAB.

FEATURES	Location/Qualifiers
source	1..532 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="TESTI4000618" /tissue_type="testis" /clone_lib="TESTI4" /note="Vector: pME18SFL3"

ORIGIN

Query Match 55.6%; Score 27.8; DB 9; Length 532;
Best Local Similarity 82.1%; Pred. No. 43;
Matches 32; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 12 ACTCCAGGACAAGGAAAACTATTTCCAATGATGATGA 50
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Db 454 AATAAAGAGCAAGGAAAACTATTTCCAATGATGATGA 492

RESULT 5

BM146766

LOCUS	BM146766	537 bp	mRNA	linear	EST 30-NOV-2001
-------	----------	--------	------	--------	-----------------

DEFINITION TCAAP1E7316 Pediatric acute myelogenous leukemia cell (FAB M1)
Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAP7316, mRNA
sequence.

ACCESSION BM146766

VERSION BM146766.1 GI:17165979

KEYWORDS EST.

SOURCE	Homo sapiens (human)
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Hominidae; Homo.

REFERENCE 1 (bases 1 to 537)

AUTHORS Wei, Y., Tsang, Y.T.M., Mei, G., Ku, J.M., Ali-Osman, F.R. Jr.,
Gunaratne, P.H., Muzny, D., Bouck, J., Gibbs, R.A. and Margolin, J.F.
TITLE Pediatric Leukemia cDNA Sequencing Project (2001)

JOURNAL Unpublished (2001)

COMMENT Contact: Dr. Judith F. Margolin
Texas Children's Cancer Center and Human Genome Sequencing Center
at Baylor College of Medicine
1102 Bates, MC3-3320 Houston, TX 77030, USA
Tel: 832-824-4536
Fax: 832-825-4038
Email: clones@txccc.org
Seq primer: M13 primer.

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FEATURES
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                /tissue_type="leukopheresis"
                /cell_type="myeloid cell"
                /dev_stage="pediatric 6 years"
                /lab_host="DH10B"
                /clone_lib="Pediatric acute myelogenous leukemia cell (FAB
M1) Baylor-HGSC project=TCAA"
                /note="Vector: lambda pSB; Site_1: BamHI; Site_2: EcoRI;
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XhoI-oligo(dT) primer [5'GGAGGACTCGAGCGGCCGAGGAG(T)VN
3'; V=A,C,G; N=A,C,G,T] and then dG tailed. Second strand
was primed with a BamHI-dC primer
[5'AGAGAGCTCGGATCCGCGGCCGCAATAATAATAAT(C) 3']".
                Double-stranded cDNA was then digested with BamHI and XhoI
                and directionally cloned into the BamHI and SalI sites of

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http://es/ScoreAccessWeb/GetItem.action?AppId=10751113&seqId=569423&ItemName=... 8/11/2006

3	27.8	55.6	4263	12	ADJ92834	Adj92834 Human co-
4	27.8	55.6	4495	14	AEC82913	Aec82913 Breast ca
5	27.8	55.6	4789	2	AAX80992	Aax80992 Human ste
6	27.8	55.6	6754	4	AAF26490	Aaf26490 Human SRC
7	27.8	55.6	6754	10	ADK67037	Adk67037 Gene #127
8	27.8	55.6	6754	14	ADY15855	Ady15855 DNA encod
9	27.8	55.6	6754	14	ADY16113	Ady16113 DNA encod
10	27.8	55.6	6754	14	ADY16117	Ady16117 DNA encod
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12	27.8	55.6	6835	2	AAV99915	Aav99915 AIB1 (Amp
13	27.8	55.6	6835	14	ADY19927	Ady19927 DNA encod
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16	27.8	55.6	7088	15	AEF22148	Aef22148 Human bas
17	27.8	55.6	7116	10	ADE53851	Ade53851 Human pro
18	27.8	55.6	7994	14	ADY16115	Ady16115 DNA encod
19	27.8	55.6	8207	10	ADF81691	Adf81691 Leukaemia
20	27.8	55.6	8207	10	ADF81690	Adf81690 Leukaemia
21	27.8	55.6	12414	14	AEA47654	Aea47654 Nucleotid
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23	26.4	52.8	403	9	ACH16713	Ach16713 Human adu
24	26.4	52.8	86453	14	ADY25730	Ady25730 SULF rela
c 25	26.4	52.8	264965	12	ADN16203	Adn16203 Human sul
c 26	26.4	52.8	268685	6	ABS56563	Abs56563 Human SUL
27	26.2	52.4	4621	2	AAV99919	Aav99919 Murine pC
28	26.2	52.4	4860	2	AAX26000	Aax26000 Murine p/
29	25	50.0	35	8	ABX11898	Abx11898 Human AIB
30	24.8	49.6	888	13	ADR63401	Adr63401 Cotton cD
c 31	24.4	48.8	1179	4	AAK87368	Aak87368 Human imm
32	24.4	48.8	3361	2	AAX80993	Aax80993 Mouse ste
c 33	24.4	48.8	171936	6	ABS56565	Abs56565 Human SUL
c 34	24.4	48.8	171936	12	ADN16205	Adn16205 Mouse sul
c 35	24.2	48.4	1664	4	AAF74192	Aaf74192 DNA encod
c 36	24.2	48.4	110000	14	AEB39174_07	Continuation (8 of
37	24.2	48.4	110000	14	AEB42737_12	Continuation (13 o
c 38	23.8	47.6	864	8	ACA36808	Aca36808 Prokaryot
c 39	23.8	47.6	10199	6	ABQ71072	Abq71072 Listeria
40	23.8	47.6	44528	6	ABA03041_29	Continuation (30 o
c 41	23.8	47.6	169659	12	ADQ59434	Adq59434 Human can
c 42	23.8	47.6	187851	14	ADZ13735	Adz13735 Human can
c 43	23.6	47.2	11614	14	AEA61172	Aea61172 Human HRA
c 44	23.6	47.2	110000	14	AEB42401_22	Continuation (23 o
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ALIGNMENTS

RESULT 1

ABX11900

ID ABX11900 standard; cDNA; 50 BP.

XX

AC ABX11900;

XX

DT 16-MAY-2003 (first entry)

XX

DE Human AIB1 delta3 isoform mRNA exon 2/exon 4 junction.

XX

KW Human; ss; exon 2/exon 4 junction; amplified in breast cancer;

KW chromosome 20q; transcription factor; antisense gene therapy; transgenic;

KW siRNA; small inhibitory RNA; cytostatic; intestinal cancer;

KW head and neck cancer; metastatic tissue cancer; neuroblastoma;

KW ovarian cancer; pancreatic cancer; prostate cancer; stomach cancer;

KW breast cancer; AIB1 delta3 isoform.

XX

OS Homo sapiens.

XX

PN WO2003003904-A2.

XX

PD 16-JAN-2003.

XX

PF 03-JUL-2002; 2002WO-US021066.

XX

PR 05-JUL-2001; 2001US-0302648P.

XX

PA (GEOU) UNIV GEORGETOWN MEDICAL CENT.

XX
 PI Riegel AT, Reiter R, Wellstein A;
 XX
 DR WPI; 2003-221517/21.
 XX
 PT New isolated AIB1 isoform as co-activator that potentiates
 PT transcriptional activity of nuclear hormone receptors, useful for the
 PT diagnosis, prevention and/or treatment of cancers, in particular breast
 PT cancer.
 XX
 PS Example 6; Fig 9; 47pp; English.
 XX
 CC The invention relates to an isolated isoform of an amplified in breast
 CC cancer 1 (AIB1) transcriptional co-activator. Also included are an
 CC isolated nucleic sequences that encodes the isoform, a vector that
 CC contains the nucleic acid, a recombinant cell that contains the nucleic
 CC acid, a diagnostic kit for the detection of cancer (comprising chemical
 CC substances that are specifically reactive to the AIB1 isoform or the
 CC nucleic acid), an anti-AIB1 isoform antibody (or antibody fragment),
 CC detection of cancer in a patient (comprising contacting a biological
 CC sample obtained from the patient with at least one chemical substance
 CC that specifically binds to the AIB1 isoform or the nucleic acid, and
 CC detecting binding), a pharmaceutical composition (comprising an agent
 CC that specifically binds to the AIB1 isoform, and prevents a co-activation
 CC of a transcription factor when administered to a patient), an siRNA
 CC (small inhibitory RNA) that inhibits expression of a transcriptional co-
 CC activator protein, a transgenic animal comprising a recombinant gene that
 CC encodes the AIB1 isoform and creating the transgenic animal. The
 CC compositions comprising the AIB1 isoform or nucleic acids that bind to
 CC the AIB1 isoform, are useful for the diagnosis, prevention and/or
 CC treatment of disorders associated with the co-activator isoforms, such as
 CC cancers of the intestines, head and neck, metastatic tissue,
 CC neuroblastoma, ovaries, pancreas, prostate, stomach, and in particular
 CC cancer of the breast. The gene for AIB1 is located on chromosome 20q. The
 CC present sequence is the junction region of the AIB1 delta3 isoform mRNA
 CC for exons 2 and 4 (unique to the delta3 isoform), which was targeted by
 CC an siRNA
 XX
 SQ Sequence 50 BP; 18 A; 9 C; 11 G; 12 T; 0 U; 0 Other;

Query Match 100.0%; Score 50; DB 8; Length 50;
 Best Local Similarity 100.0%; Pred. No. 3e-09;
 Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCCATGTGATACTCCAGGACAAGGGAAAACTATTTCCAATGATGATGA 50
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RESULT 2

ADV43475

ID ADV43475 standard; cDNA; 4239 BP.

XX

AC ADV43475;

XX

DT 10-MAR-2005 (first entry)

XX

DE Human psychoneuroendocrinimmune expressed sequence tag SEQ ID NO 1103.

XX

KW microarray; psychoneuroendocrinimmune; chronic fatigue;

KW non-insulin dependent diabetes; allergy; immune disorder; inflammation;

KW cancer; neoplasm; infection; expressed sequence tag; ss.

XX

OS Homo sapiens.

XX

PN WO2004108899-A2.

XX

PD 16-DEC-2004.

XX

PF 04-JUN-2004; 2004WO-US017686.

XX

PR 04-JUN-2003; 2003US-0475915P.

XX

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX

PI Nicholson A, Vernon SD;

Qy 12 ACTCCAGGACAAGGGAAAACTATTTCCAATGATGATGA 50
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Db 243 AATAAAGAGCAAGGAAAACTATTTCCAATGATGATGA 281

ADJ92834

http://es/ScoreAccessWeb/GetItem.action?AppId=10751113&seqId=569423&ItemName=... 8/11/2006

